

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: LaBrie, Samuel T.
Lal, Preeti
Murry, Lynn E.

(ii) TITLE OF THE INVENTION: NOVEL TUBBY HOMOLOGUE

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Dr.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0232US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HNT2NOT01
(B) CLONE: Concensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Ala Ser Arg Cys Arg Leu Ser Pro Ser Gly Asp Ser Val Phe
 1 5 10 15
 His Glu Glu Met Met Lys Met Arg Gln Ala Lys Leu Asp Tyr Gln Arg
 20 25 30
 Leu Leu Leu Glu Lys Arg Gln Arg Lys Lys Arg Leu Glu Pro Phe Met
 35 40 45
 Val Gln Pro Asn Pro Glu Ala Arg Leu Arg Arg Ala Lys Pro Arg Ala
 50 55 60
 Ser Asp Glu Gln Thr Pro Leu Val Asn Cys His Thr Pro His Ser Asn
 65 70 75 80
 Val Ile Leu His Gly Ile Asp Gly Pro Ala Ala Val Leu Lys Pro Asp
 85 90 95
 Glu Val His Ala Pro Ser Val Ser Ser Val Val Glu Glu Asp Ala
 100 105 110
 Glu Asn Thr Val Asp Thr Ala Ser Lys Pro Gly Leu Gln Glu Arg Leu
 115 120 125
 Gln Lys His Asp Ile Ser Glu Ser Val Asn Phe Asp Glu Glu Thr Asp
 130 135 140
 Gly Ile Ser Gln Ser Ala Cys Leu Glu Arg Pro Asn Ser Ala Ser Ser
 145 150 155 160
 Gln Asn Ser Thr Asp Thr Gly Thr Ser Gly Ser Ala Thr Ala Ala Gln
 165 170 175
 Pro Ala Asp Asn Leu Leu Gly Asp Ile Asp Asp Leu Glu Asp Phe Val
 180 185 190
 Tyr Ser Pro Ala Pro Gln Gly Val Thr Val Arg Cys Arg Ile Ile Arg
 195 200 205
 Asp Lys Arg Gly Met Asp Arg Gly Leu Phe Pro Thr Tyr Tyr Met Tyr
 210 215 220
 Leu Glu Lys Glu Glu Asn Gln Lys Ile Phe Leu Leu Ala Ala Arg Lys
 225 230 235 240
 Arg Lys Lys Ser Lys Thr Ala Asn Tyr Leu Ile Ser Ile Asp Pro Val
 245 250 255
 Asp Leu Ser Arg Glu Gly Glu Ser Tyr Val Gly Lys Leu Arg Ser Asn
 260 265 270
 Leu Met Gly Thr Lys Phe Thr Val Tyr Asp Arg Gly Ile Cys Pro Met
 275 280 285
 Lys Gly Arg Gly Leu Val Gly Ala Ala His Thr Arg Gln Glu Leu Ala
 290 295 300
 Ala Ile Ser Tyr Glu Thr Asn Val Leu Gly Phe Lys Gly Pro Arg Lys
 305 310 315 320
 Met Ser Val Ile Ile Pro Gly Met Thr Leu Asn His Lys Gln Ile Pro
 325 330 335
 Tyr Gln Pro Gln Asn Asn His Asp Ser Leu Leu Ser Arg Trp Gln Asn
 340 345 350
 Arg Thr Met Glu Asn Leu Val Glu Leu His Asn Lys Ala Pro Val Trp
 355 360 365
 Asn Ser Asp Thr Gln Ser Tyr Val Leu Asn Phe Arg Gly Arg Val Thr
 370 375 380
 Gln Ala Ser Val Lys Asn Phe Gln Ile Val His Lys Asn Asp Pro Asp
 385 390 395 400
 Tyr Ile Val Met Gln Phe Gly Arg Val Ala Asp Asp Val Phe Thr Leu
 405 410 415
 Asp Tyr Asn Tyr Pro Leu Cys Ala Val Gln Ala Phe Gly Ile Gly Leu
 420 425 430
 Ser Ser Phe Asp Lys Arg Ile Gln Thr Leu Arg Met Gln Glu Leu Cys
 435 440 445
 Glu Leu His Arg Gln His His Ser Ala Ala Ser Leu Val His Arg Thr
 450 455 460
 Ala Cys Gln Arg Trp Val Gly His Pro Trp Arg Gln Leu Pro Gln Ser
 465 470 475 480
 Ser Leu Val Gly Pro Asp Leu Xaa Leu His Met

485

490

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HNT2NOT01
- (B) CLONE: Concensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCACGAGGTG	GGGGCTTTC	TCGGTGGCGG	GCATGGAGGC	TTCGCGCTGC	CCGCTCAGTC	60
CCAGCGCGA	CAGTGTCTTC	CATGAAGAAA	TGATGAAGAT	GCGACAGGCT	AACCTGGATT	120
ATCAGAGGCT	ACTACTTGAG	AAGAGGCAAA	GGAAAAAGCG	CCTTGAGCCA	TTTATGGTGC	180
AGCCCAATCC	AGAAGGCCAGG	CTACGTGGG	CAAAGCCAAG	GGCCAGTGAT	GAGCAGACTC	240
CCTTGGTGA	CTGTCTACT	CCCCACAGCA	ATGTCATCTT	ACATGGTATT	GATGGTCCAG	300
CTGCTGTCT	GAAACCCAGAC	GAAGTCATG	CTCCATCAGT	AAGCTCTCT	GTTGTGGAAG	360
AAGATGCTGA	AAACACCGTG	GATACTGCTT	CCAAGCCAGG	ACTTCAGGAG	CGTCTCCAAA	420
AGCATGATAT	CTCTGAAAGT	GTGAACCTCG	ATGAGGAGAC	TGATGGAATA	TCCCCAGTCAG	480
CATGTTAGA	AAGACCCAAT	TCTGCATCAA	GCCAGAAATTC	AACCGATACA	GGCACTTCCG	540
GTTCTGCTAC	TGCCGCCCAA	CCAGCTGATA	ACCTCCTGGG	AGACATAGAC	GACCTGGAGG	600
ACTTTGTGTA	TAGTCCTGCC	CCTCAAGGTG	TCACAGTAAG	ATGTCGGATA	ATCCGGGATA	660
AAAGGGGAAT	GGATCGGGGT	CTCTTCCCCA	CCTACTATAT	GTACTTGGAA	AAAGAAGAAA	720
ATCAGAAAGAT	ATTCTCTTCTT	GCAGCTAGAA	AGCGGAAAAA	GAGCAAACAA	GCCAACCTACC	780
TTATCTCCAT	TGATCCAGTT	GATTTATCTC	GTGAAGGAGA	AAGTTATGTC	GGCAAGCTTA	840
GATCCAACCT	CATGGGGACC	AAGTTTACAG	TTTATGACCG	TGGCATCTGC	CCCATGAAAGG	900
GCCGGGGTTT	GGTAGGGAGCG	GCCCCACACCC	GGCAGGAGCT	GGCTGCCATC	TCCTATGAAA	960
CAAACGTACT	TGGATTAAA	GGTCCTAGGA	AAATGCTGT	GATCATTCCT	GGAAATGACAC	1020
TGAATCATAA	GGAGATCCCC	TATCAGCCAC	AAAACAACCA	TGACAGTTG	CTCTCAAGGT	1080
GGCAGAACAG	AATATGGAA	AATCTGGTTG	AGCTGCACAA	CAAGGGCCCC	GTCTGGAACA	1140
GTGACACTCA	GTCCTATGTC	CTCAACTTCC	GTGGCCGGGT	CACTCAGGCG	TCTGTGAAGA	1200
ACTTCACAGAT	AGTCCACAAA	AATGACCCCTG	ATTATATAGT	CATGCAGTTT	GGACGTGTGG	1260
CAGATGACGT	GTTCACACTG	GATTACAAT	ACCCACTTTC	TGCAGTACAG	GCCTTTGGCA	1320
TCGGTCTTTC	TAGCTTTGAC	AAACGTATCC	AAACCTTGAG	AATGCAGGAG	CTCTGTGAGC	1380
TCCACCGTCA	GCACCAATTCA	GCTGCATCCC	TTGTGCACAG	GACTGCCTGC	CAGCGTTGGG	1440
TGGGACACCC	GTGGCGGCAG	CTCCCTCAGT	CTTCCCTTGT	CGGCCCTGAC	CTNTNACTAC	1500
ATATGTAGNA	CCCCGAGACC	AAAAAA				1525

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1279766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Ser Lys Pro His Ser Asp Trp Ile Pro Tyr Ser Val Leu Asp
 1 5 10 15
 Asp Glu Gly Ser Asn Leu Arg Gln Gln Lys Leu Asp Arg Gln Arg Ala
 20 25 30
 Leu Leu Glu Gln Lys Gln Lys Lys Arg Gln Glu Pro Leu Met Val
 35 40 45
 Gln Ala Asn Ala Asp Gly Arg Pro Arg Ser Arg Arg Ala Arg Gln Ser
 50 55 60
 Glu Glu Gln Ala Pro Leu Val Glu Ser Tyr Leu Ser Ser Ser Gly Ser
 65 70 75 80
 Thr Ser Tyr Gln Val Gln Glu Ala Asp Ser Ile Ala Ser Val Gln Leu
 85 90 95
 Gly Ala Thr Arg Pro Pro Ala Pro Ala Ser Ala Lys Lys Ser Lys Gly
 100 105 110
 Ala Ala Ala Ser Gly Gly Gln Gly Ala Pro Arg Lys Glu Lys Lys
 115 120 125
 Gly Lys His Lys Gly Thr Ser Gly Pro Ala Thr Leu Ala Glu Asp Lys
 130 135 140
 Ser Glu Ala Gln Gly Pro Val Gln Ile Leu Thr Val Gly Gln Ser Asp
 145 150 155 160
 His Asp Lys Asp Ala Gly Glu Thr Ala Ala Gly Gly Ala Gln Pro
 165 170 175
 Ser Gly Gln Asp Leu Arg Ala Thr Met Gln Arg Lys Gly Ile Ser Ser
 180 185 190
 Ser Met Ser Phe Asp Glu Asp Glu Asp Glu Asn Ser Ser Ser
 195 200 205
 Ser Ser Gln Leu Asn Ser Asn Thr Arg Pro Ser Ser Ala Thr Ser Arg
 210 215 220
 Lys Ser Ile Arg Glu Ala Ala Ser Ala Pro Ser Pro Ala Ala Pro Glu
 225 230 235 240
 Pro Pro Val Asp Ile Glu Val Gln Asp Leu Glu Glu Phe Ala Leu Arg
 245 250 255
 Pro Ala Pro Gln Gly Ile Thr Ile Lys Cys Arg Ile Thr Arg Asp Lys
 260 265 270
 Lys Gly Met Asp Arg Gly Met Tyr Pro Thr Tyr Phe Leu His Leu Asp
 275 280 285
 Arg Glu Asp Gly Lys Lys Val Phe Leu Leu Ala Gly Arg Lys Arg Lys
 290 295 300
 Lys Ser Lys Thr Ser Asn Tyr Leu Ile Ser Val Asp Pro Thr Asp Leu
 305 310 315 320
 Ser Arg Gly Gly Asp Ser Tyr Ile Gly Lys Leu Arg Ser Asn Leu Met
 325 330 335
 Gly Thr Lys Phe Thr Val Tyr Asp Asn Gly Val Asn Pro Gln Lys Ala
 340 345 350
 Ser Ser Ser Thr Leu Glu Ser Gly Thr Leu Arg Gln Glu Leu Ala Ala
 355 360 365
 Val Cys Tyr Glu Thr Asn Val Leu Gly Phe Lys Gly Pro Arg Lys Met
 370 375 380
 Ser Val Ile Val Pro Gly Met Asn Met Val His Glu Arg Val Cys Ile
 385 390 395 400
 Arg Pro Arg Asn Glu His Glu Thr Leu Leu Ala Arg Trp Gln Asn Lys
 405 410 415
 Asn Thr Glu Ser Ile Ile Glu Leu Gln Asn Lys Thr Pro Val Trp Asn
 420 425 430
 Asp Asp Thr Gln Ser Tyr Val Leu Asn Phe His Gly Arg Val Thr Gln
 435 440 445
 Ala Ser Val Lys Asn Phe Gln Ile Ile His Gly Asn Asp Pro Asp Tyr
 450 455 460
 Ile Val Met Gln Phe Gly Arg Val Ala Glu Asp Val Phe Thr Met Asp
 465 470 475 480
 Tyr Asn Tyr Pro Leu Cys Ala Leu Gln Ala Phe Ala Ile Ala Leu Ser

485	490	495
Ser Phe Asp Ser Lys Leu Ala Cys Glu		
500	505	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1305497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Ser Lys Pro His Ser Asp Trp Ile Pro Tyr Ser Val Leu Asp			
1	5	10	15
Asp Glu Gly Arg Asn Leu Arg Gln Gln Lys Leu Asp Arg Gln Arg Ala			
20	25	30	
Leu Leu Glu Gln Lys Gln Lys Lys Arg Gln Glu Pro Leu Met Val			
35	40	45	
Gln Ala Asn Ala Asp Gly Arg Pro Arg Ser Arg Arg Ala Arg Gln Ser			
50	55	60	
Glu Glu Gln Ala Pro Leu Val Glu Ser Tyr Leu Ser Ser Ser Gly Ser			
65	70	75	80
Thr Ser Tyr Gln Val Gln Glu Ala Asp Ser Leu Ala Ser Val Gln Leu			
85	90	95	
Gly Ala Thr Arg Pro Thr Ala Pro Ala Ser Ala Lys Arg Thr Lys Ala			
100	105	110	
Ala Ala Thr Ala Gly Gly Gln Gly Ala Ala Arg Lys Glu Lys Lys			
115	120	125	
Gly Lys His Lys Gly Thr Ser Gly Pro Ala Ala Leu Ala Glu Asp Lys			
130	135	140	
Ser Glu Ala Gln Gly Pro Val Gln Ile Leu Thr Val Gly Gln Ser Asp			
145	150	155	160
His Ala Gln Asp Ala Gly Glu Thr Ala Ala Gly Gly Gly Glu Arg Pro			
165	170	175	
Ser Gly Gln Asp Leu Arg Ala Thr Met Gln Arg Lys Gly Ile Ser Ser			
180	185	190	
Ser Met Ser Phe Asp Glu Asp Glu Glu Asp Glu Glu Asn Ser Ser			
195	200	205	
Ser Ser Ser Gln Leu Asn Ser Asn Thr Arg Pro Ser Ser Ala Thr Ser			
210	215	220	
Arg Lys Ser Val Arg Glu Ala Ala Ser Ala Pro Ser Pro Thr Ala Pro			
225	230	235	240
Glu Gln Pro Val Asp Val Glu Val Gln Asp Leu Glu Glu Phe Ala Leu			
245	250	255	
Arg Pro Ala Pro Gln Gly Ile Thr Ile Lys Cys Arg Ile Thr Arg Asp			
260	265	270	
Lys Lys Gly Met Asp Arg Gly Met Tyr Pro Thr Tyr Phe Leu His Leu			
275	280	285	
Asp Arg Glu Asp Gly Lys Lys Val Phe Leu Leu Ala Gly Arg Lys Arg			
290	295	300	
Lys Lys Ser Lys Thr Ser Asn Tyr Leu Ile Ser Val Asp Pro Thr Asp			
305	310	315	320
Leu Ser Arg Gly Gly Asp Ser Tyr Ile Gly Lys Leu Arg Ser Asn Leu			

	325	330	335												
Met	Gly	Thr	Lys	Phe	Thr	Val	Tyr	Asp	Asn	Gly	Val	Asn	Pro	Gln	Lys
	340				345									350	
Ala	Ser	Ser	Ser	Thr	Leu	Glu	Ser	Gly	Thr	Leu	Arg	Gln	Glu	Leu	Ala
	355				360							365			
Ala	Val	Cys	Tyr	Glu	Thr	Asn	Val	Leu	Gly	Phe	Lys	Gly	Pro	Arg	Lys
	370			375						380					
Met	Ser	Val	Ile	Val	Pro	Gly	Met	Asn	Met	Val	His	Glu	Arg	Val	Ser
	385			390					395				400		
Ile	Arg	Pro	Arg	Asn	Glu	His	Glu	Thr	Leu	Leu	Ala	Arg	Trp	Gln	Asn
	405							410				415			
Lys	Asn	Thr	Glu	Ser	Ile	Ile	Glu	Leu	Gln	Asn	Lys	Thr	Pro	Val	Trp
	420						425				430				
Asn	Asp	Asp	Thr	Gln	Ser	Tyr	Val	Leu	Asn	Phe	His	Gly	Arg	Val	Thr
	435						440				445				
Gln	Ala	Ser	Val	Lys	Asn	Phe	Gln	Ile	Ile	His	Gly	Asn	Asp	Pro	Asp
	450						455				460				
Tyr	Ile	Val	Met	Gln	Phe	Gly	Arg	Val	Ala	Glu	Asp	Val	Phe	Thr	Met
	465						470			475				480	
Asp	Tyr	Asn	Tyr	Pro	Leu	Cys	Ala	Leu	Gln	Ala	Phe	Ala	Ile	Ala	Leu
									485		490				495
Ser	Ser	Phe	Asp	Ser	Lys	Leu	Ala	Cys	Glu						
					500				505						